REMARKS

Reconsideration and allowance are respectfully requested.

Claims 24 and 27-36 are now pending, with Claim 24 being the sole independent claim.

No amendments are being submitted herewith.

Applicants gratefully acknowledge the withdrawal of the Final Office Action mailed August 18, 2005.

Turning now to the rejections of the Non-Final Office Action mailed November 22, 2005:

Regarding the Section 112, 1st paragraph (written description) rejection, Applicants respectfully traverse.

Applicants submit that the specification discloses to one of ordinary skill in the art a representative number of polynucleotides encoding viral movement polypeptides with at least 95% sequence identity to SEQ ID NO:6 and not just a single polynucleotide encoding SEQ ID NO:6.

The specification at page 6, line 34 to page 7, line 8, discloses alterations in nucleotide sequence that are not expected to alter functionality, such as alterations that produce a chemically equivalent amino acid at a given site or alterations in the N- or C-terminal portions.

Thus, from the foregoing, the skilled artisan would immediately understand the specification to disclose a representative number of polynucleotide sequences, having different nucleotide substitutions, encoding viral movement proteins that vary within at least 95% sequence identity of SEQ ID NO:6.

In addition, Applicants submit that the specification includes a sufficient and adequate disclosure to convince a person of skill in the art, having knowledge of what has come before, that Applicants possessed the invention as recited in Claims Claims 24 and 27-36.

Applicants submit that one of ordinary skill would have within his or her knowledge Xoconostle-Cazares et al. (1999, Science 283, 94-98, copy previously submitted).

Xoconostle-Cazares et al. discloses a plant paralog to a viral movement protein that potentiates transport of mRNA into phloem. To identify such paralogs within the phloem sap of pumpkin, Xoconostle-Cazares et al. used polyclonal antibodies raised against the plant viral movement protein from red clover.

Attached hereto as Appendix A is an alignment of SEQ ID NO:6 of the pending claims with CmPP16-2 (gi: 4164540), one of the movement proteins from pumpkin identified by Xoconostle-Cazares et al. Amino acids conserved among all sequences are indicated with an asterisk (*) on the top row; conservative amino acid changes

are indicated by an arrow above the conservative amino acid changes; dashes are used by the program to maximize alignment of the sequences.

A PKC-like C_2 Ca^{2+} /phospholipids-binding domain as disclosed in Xoconostle-Cazares et al. is underlined on Appendix A.

The sequences from corn and pumpkin are similar in length (120-130 amino acid residues) and share 24.5% sequence identity, based on the Clustal method of alignment, which is raised to 60% similarity after the inclusion of conservative amino acid changes. Furthermore, substantial sequence similarity exists between the two sequences in a PKC-like C_2 Ca^{2+} /phospholipids-binding domain as disclosed in Xoconostle-Cazares et al. The isolated protein from pumpkin displays functional similarity and a sequence identity of about 14.7%, based on the Clustal method of alignment, to the movement protein from red clover, which is less than the sequence identity shared between the pumpkin sequence and SEQ ID NO:6.

Applicants submit that one of ordinary skill, upon reading the instant specification, would readily recognize that the inventors were in possession of and had invented a polynucleotide sequence encoding a viral movement polypeptide having an amino acid sequence of at least 95% sequence identity to SEQ ID NO:6, since this person of ordinary skill would have had the knowledge of Xoconostle-Cazares et al. as explained above, would readily obtain the information illustrated in Appendix A and the percent identity of the sequences therein, and therefore in combination with the instant specification would readily recognize where amino acid substitutions could be made to result in a polypeptide having an amino acid sequence of at least 95% sequence identity to SEQ ID NO:6 while still retaining viral movement functionality.

Withdrawal of the Section 112, 1st paragraph (written description) rejection is respectfully requested.

Regarding the Section 101 (utility) rejection, Applicants respectfully traverse.

As an initial matter, Applicants understand the sole basis of this utility rejection to be that the specified utility of the claims is not credible. That is, Applicants do not understand this utility rejection to be based on the specific and substantial credibility prongs, since no reasons have been given as to why these two prongs are not supported. The only reasons provided focus on establishing that the claimed invention does not have viral movement functionality.

Applicants submit that the above remarks with respect to the Section 112, 1st paragraph (written description) rejection and the remarks below with respect to the Section 112, 1st paragraph (enablement) rejection are applicable here. In view of these remarks, Applicants submit that it is credible that the claimed invention has viral movement functionality.

Therefore, withdrawal of the Section 101 (utility) rejection is respectfully requested.

Regarding the Section 112, 1st paragraph (enablement) rejection, Applicants respectfully traverse.

The remarks above with respect to the Section 112, 1st paragraph (written description) rejection are applicable here. As discussed supra, the specification, coupled with knowledge about viral movement protein functionality and structure, provides sufficient guidance to one of ordinary skill as to which amino acids could be modified to result in a polypeptide sequence having at least 95% identity to SEQ ID NO:6 of the present application while still maintaining viral movement functionality. Furthermore, the experimentation needed to determine functionality is not undue in this field. Applicants disclose methods for expressing the recombinant constructs in monocot, dicot and microbial cells (see prophetic Examples 4-6 of the instant specification). Xoconostle-Cazares et al., for example, discloses various methods for assessing viral movement protein functionality. Applicants submit that one of ordinary skill in the art could carry out these methods without undue experimentation.

In view of the foregoing, Applicants respectfully request withdrawal of the Section 112, 1st paragraph (enablement) rejection.

Applicants believe that the foregoing is responsive to each of the points recited in the Non-Final Office Action mailed November 22, 2005, and submit that the present application is in allowable form. Favorable consideration and passage to issue are solicited.

The Commissioner is authorized to charge Deposit Account No. 18-2284 (DLA Piper Rudnick Gray Cary US LLP) for any requisite fees due or to credit any overpayment.

Respectfully submitted,

J. KENNETH JOUNG
ATTORNEY FOR APPLICANTS
REGISTRATION NO. 41,881
TELEPHONE: 312-368-7049
FACSIMILE: 312-630-7417

Dated: 22 March 2006

Response to Non-Final Office Action
Application No.: 09/913,569
Docket No.: BB-1344

APPENDIX A

Appendix A shows a comparison of the amino acid sequences of the corn viral movement protein (SEQ ID NO:6) and the movement protein from pumpkin (gi: 4164540). Identical amino acids are indicated with an asterix (*) above the alignment. Conservative amino acid changes are indicated by an arrow (^) above the conservative changes. Dashes are used by the program to maximize alignment of the sequences. A PKC-like C_2 Ca^{2+} /phospholipids-binding domain as disclosed in Xoconostle-Cazares et al. (1999, Science 283, 94-98) is underlined.

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                 *  * ^** *^^^***^  * * ^ ^**** ^^ ^^**v * ^*   *  * ***^* *

SEQ ID NO:6      MVHGTLEVLLVGAKGLENTDYLCN-MDPYAILKCRSQEQKSSIATGKGTTPEWNENFIFT
Gi:4164540       MGMGMMEVHLISGKGLQAHDPLNKPIDPYAEINFKGQERMSKVAKNAGPDPIWNEKFKFL

                 *    ^^    ^^ *^** *^   ** ^*^  * ^  ^ ^*         ^** ^*^*^
SEQ ID NO:6      VSDRTTD----LVIKLMDSDTGTADDFVGEATIPLEAVYTE------RSIPPTLYNVVKG
Gi:4164540       VEYPGSGGDFHILFKVMDHDAIDGDDYIGDVKIDVQNLLAEGVRKGWSELPPRMYQVLAH

                   *  *** **^ *  ^            *
SEQ ID NO:6      EKYC-GEIKVGLTFTPEDTRQRGLPEDFGGWKQSS
Gi:4164540       KIYFKGEIEVGVFFQRQ-----------GRIGIN
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